

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: US1091932,888B

Source: TFW16

Date Processed by STIC: 12-3-04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/03/2004

PATENT APPLICATION: US/09/932,888B

TIME: 10:39:30

Input Set : A:\LL31 12-0016 sequence listing.txt

Output Set: N:\CRF4\12032004\I932888B.raw

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3 <110> APPLICANT: PURINA MILLS, LLC
4   PURDUE RESEARCH FOUNDATION
6 <120> TITLE OF INVENTION: PORCINE LEPTIN PROTEIN, ANTISENSE AND ANTIBODY
8 <130> FILE REFERENCE: LL31.12-0016
10 <140> CURRENT APPLICATION NUMBER: US 09/932,888B
11 <141> CURRENT FILING DATE: 2001-08-20
13 <150> PRIOR APPLICATION NUMBER: US 08/692,922
14 <151> PRIOR FILING DATE: 1996-07-31
16 <160> NUMBER OF SEQ ID NOS: 11
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 5917
22 <212> TYPE: DNA
23 <213> ORGANISM: Sus scrofa
26 <220> FEATURE:
27 <221> NAME/KEY: gene
28 <222> LOCATION: (1)..(5917)
29 <223> OTHER INFORMATION: Nucleotide sequence of the porcine leptin gene. CDS Location:
30   join (942..1085,3400..3753)
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <222> LOCATION: (2943)..(2944)
35 <223> OTHER INFORMATION: n is a, c, g, or t
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: (2983)..(2983)
40 <223> OTHER INFORMATION: n is a, c, g, or t
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (3037)..(3037)
45 <223> OTHER INFORMATION: n is a, c, g, or t
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50 caatacccag cccaggggag cctcttcca gggagccccg cttgtactcc tgagatgtca      120
52 tgtccttctt gcagagctct tcctcacggc atcgggacgg cggttcaccc ttttgcctct      180
54 ccggataaac tgtaagctac ttgagagcag agaacatcca ttgttcgctg tggcatccgt      240
56 ggtacctagc acggcatctg acatattatc agatcttcca caaaggccag tttacggttg      300
58 aatgcccggt gaattcaggc tcccagtgga agagcgagga agtaataaag ccggtgataa      360
60 atgccgcggt ggagacacca gcgggctgcc gtgagactaa tggagaggac agtaacgtta      420
62 tctctaatac gaggggtggt atagagtaca ttctataaca cctttaaagc tctttcacac      480
64 gcattatcca atttgatcct cataaaagcc tggagatgtg tatattgtgg tggatggagg      540
66 gggagtcttt agcagttatg ggatatgcct gaagtcgtgc agctagtaaa tggctggatt      600
68 caaaccagac ctcaaaagcc tgcctgtttg ctcatgcccc ctgccccgac tgcccactct      660

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70 gtggcccaca gcacaactca ccgtcgtctt cttgatccgt tttcttgatc cggtctgtgt 720
72 ctccccaagg aatgcttttc attaacatat gtctaggtaa tgaattatct tgactctgag 780
74 gaggccatag cacatgccgt aacgcgacag ctcccttgat ctgcatctga ggctgtggct 840
76 ggtaacgggc gtggggaggg ggcgttcgct gagaccccag ggacacgcca tgtgtgggtc 900
78 cctctgtttc caggccccag aagcacatcc cggaaaggaa aatgcgctgt ggaccctgt 960
80 gccgattcct gctggctttg gcctatctgt cctacgttga agccgtgccc atctggagag 1020
82 tccaggatga caccaaaacc ctcatcaaga cgattgtcac caggatcagt gacatttcac 1080
84 acatggtagg gaaggcctgg gagacaaggc cgaacctgtg gccagcccs ggggaggagg 1140
86 ggtaccggac ctacagaggt ggcgagggtg ggaagggtcg gcggtggcct tgacgcctcc 1200
88 cccaccccc ccaaccagct gcctttgtct ctccgcttcc ctaccgcac cccccacgt 1260
90 cttatctct cttcttccca gactggaata ctgatgccca ggactagagg aagccctaaa 1320
92 ggtcctgtgt gcctttgcca ggtgcgcaga ccccccagca tcacccctc tggcctccat 1380
94 cacgtctccg gaatgttcta atctgtagga attcttctcg gtgacagctg aactctgacc 1440
96 ctgcggacgc cccttactgc tagtctgccc cattgagcct ttttctctat acaacctct 1500
98 acatgtttgc aaactttct caatgtcccc aggggtgttt ctctggggtc cgcaggccga 1560
100 gaccttcagc ctcttctcag ctgaggtccg tctttagaat tcagaagacg aggtgtgact 1620
102 cctcaccctg ctgttccctc tctgtaaaat ctcaagcacg ttaagtcctt ccgtgtctga 1680
104 aaccttagtt tccctcatcc agataatggg actgttactg ggaagatgtt accggaatcc 1740
106 agggctcttg ctcatggagc tcaagaatga acttggcgaa cgcacaggga gccgagcaag 1800
108 cagaagtctt tattacagga aggcagacag ctcccagcac agacacgggg agggaagagt 1860
110 ccccccgcgc attgttctac ggaggttttt atcacttaaa gacgggagta ccaatgtggg 1920
112 gtccagatat ccgttcttct tcccattgcc cagtttacct atatggcgcc ttgtccagga 1980
114 gggactctgt agagttaggg gtgctccgta agttttatgg tgcgtctgct cttctctgcc 2040
116 ctgacttag agtcgccact ctttccattc ttctgtcac agtcaaatgc ataggtcagg 2100
118 ggtaattcc cacttcaca gaaatcaaat gtctttcaa tagttaatct tccaataagc 2160
120 aaggcctgct tgtcttgatt agtttttaca aatcttaaac catggccatt aatcaggga 2220
122 gagatcgaag cccatgttcc cacactaact gcctgaatta ttagtctgcc tcaggactat 2280
124 cttaatagtc ttcgcaagg tgttttgaga ttaaattaga taggagttcc tgtcgaggcg 2340
126 cgacggaaac agatccgact cagaaccatg agacagggtc gatccctggc tttgtcagt 2400
128 ggttaggata tgggtgctgt gtgagctgtg gtgtaggctg cagaggtggc tcggatcccg 2460
130 cgttgctgtg gctgtggtgt aggcgggtgc agacagctcc gattagacc ctagcctggg 2520
132 aacctccatg tgccgcgggt accgctaaaa aaagacaaaa gatggaaaaa aaaaaggtta 2580
134 cattagataa agcaagtgc tctccacca ccacacatat cctgcagaa ccaggacaga 2640
136 gcatgccttc ttgaaaagtt ttcggttggt gctttgatag caccagcct taaaagccag 2700
138 cttttcaatc tgcccagagc agtctggaga ctccgcac tctggccac tctgagttc 2760
140 taacagtggc cttggcgagc ctgggagcag tccggtggcc agaagcaggg acagctgaga 2820
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144 aacagctgcg catgacagat ccagcgtgtc ccagcctgtg tggtcaggg agtgaygtg 2940
V--> 146 cgnnyaggy gygggggagc tgaggagcga ggcggggcat cngggggctg cagcctccat 3000
V--> 148 ccctaagtgg ggagacttca tgaagagcct gaccagnagg gaggggcatg tgtggaggac 3060
150 ctacaggcct ggggaaggct agacccaact atgtgagaaa cagacagtcg tggctggttc 3120
152 tcagaagag gcatctggag gccattcgaa tgcccaaagc tgtctgggtg aggcagggtc 3180
154 tagtaggcag aagacagaag ccgctggagc cagcttggag gcttggcagc cagccagcc 3240
156 caaggagttc gggcctagat aggattgtgt ggaaggggaa gaggcagccg gaggtggggg 3300
158 gtgggggtgg acccgtctcc acgctgcag gaaggccagg ggctgcagag ccaacatctc 3360
160 tctcgtgag cgtctcgtct tccccttct cctgcacagc agtctgtctc ctccaaacag 3420
162 agggtcaccg gtttggaact catccctggg ctccatctg tctgagttt gtccaagatg 3480
164 gaccagacc tggcgatcta ccaacagatc ctaccagtc tgccttcag aaatgtgatc 3540
166 caaatatcga atgacctgga gaacctccgg gaccttctcc acctgctggc ctctccaag 3600

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168 agctgcccct tgcccagcag ggccttggag accttggaga gcctgggagg cgctcctggaa 3660
170 gcctccctct actccacgga ggtgggtggcc ctgagcaggc tgcagggggc tctgcaggac 3720
172 atgctgcggc agctggacct cagccctggc tgctgaagcc ttgaaggcct ctctccccac 3780
174 agtcggggga agaaacctga gcttccagga gtctgctgga gaagagagcc tgtgcggacc 3840
176 tcctctctgc aggtctgcgg accatttctc tctcgtctcg ctaagctgct cttccaaagg 3900
178 cagaaaactc caaggcacga caccaaagac agaaaggcct gggtccgcgc ccaccggaaa 3960
180 gggggcgccg tccagccaac ggtggactag atttcggatt ttccaccaac gtcttccttc 4020
182 ctgttccatc tccagctcac cgcgtgcttc agcgtgaccg gggggatttc agagcctttc 4080
184 gaccatcaag cagggttcca tctgagaatt ccggggagca cgggtgaaggc tacaggcaca 4140
186 cacagctgga tgctcccacg caacacaagt tggaagcatt tctttattta ttatgcggtg 4200
188 tattctgggt ggatttgaag caaaacacca gcctttccag gctctctggg gtcagccggg 4260
190 gctaggggga ggctcccgag gtgctgtttc cagtaccatc catgggcctg ctgaggccaa 4320
192 cccattttga gtgacttgag ggctctcaag gtcgttctct agagactggc ttgtttcta 4380
194 ctgtgactga ctttaaaact gcagcgtgtg cactggcatc gcctgcgcgg atctcgaagg 4440
196 gccaggttct cttagaaaga agaagatgaa ctttgtcagg ggtgtgtacg cggagacagg 4500
198 aagtgtgttg gtgggcgggg catggatcca gaatgtgtat ttcttgttg atggacattt 4560
200 gtgtgagggg ctctctggac aggggtgaggt cattgtctca tcttcgtggg ttcatgaga 4620
202 gaaggagatg attccttcac gggggtcgtg gggttttgcc agccgcccg gcaggagtgg 4680
204 ggaaggggct gaagccgaag accgttgggg gccgtggtga gctctgcctt ctccagctgc 4740
206 tagaggctgg tctttctcat caggagtgga gggctctcgc ttggagacag tgatccccag 4800
208 ggcgggatcc ttgccgtggc cctctgaatg gtctgggtga tcccacactg atgtcataac 4860
210 agggaaagtgc cctggtttgg gatttgtatg ctcacccaaa gcaagggcct gcttcccatc 4920
212 cattttggga aggatttttt ctccaggggg aggggtgaaag ctctgggagg tctgtgggct 4980
214 tacgagatgg tccaagtctt gggtcagtga gtcccgggac tcgtgaccgc ctcgaggagc 5040
216 ccccttctcc ctacaggtca tgttcaatag gtcaaacaag gaggcatggg tttccaccat 5100
218 cctgccgctg tgatgcagcc atcgactac aggaggtaga tctgtccaag gaaatttgaa 5160
220 tctcaagcaa tcactttcaa gactgagcat ctattgtgct cagccccaac tgggtgctatg 5220
222 ggctcagaga agctcatcaa ataaatatta aaatccagtc ctgccttcag gaccttgcat 5280
224 tccagatgat aacacctccc ccacaccccg tctgcagagg ctgtcatttc accatggcaa 5340
226 ccgagcagct gaaacacagt gcggctctca gcagggtgaa aggctgagct gaggagggca 5400
228 gtgcccgggc ccacaggcta accctgcttg cacttggtag catttttact gttcggggcg 5460
230 catcagcatc tattactgag aagccgcatc cctttgaagc aggatagctg agactataaa 5520
232 aataagaaaa taccagagtt cccttgtggc acagagggct aaggatccag tgttgttgc 5580
234 gcagcagctt gggtcacggc tgtggcaagg gttcgatccc tggcctggga actttcacat 5640
236 gttgcaggca aggccaaaaa aaaataaata aataaaaaa aacaaaaaaa aacaagacca 5700
238 taacagcaga ctggtggcaa accaggacta gaacctgggt cctctgaccc ctagagtcag 5760
240 tgtcccctga gccagctagt gttctctggg gacgggaaca ggggtgggca gggagttcag 5820
242 gaagtgtttg ctggaagagc ggagtttcca ggctgatttt gcaggagggtg agggaaagtgg 5880
244 attgcctgga gggaggaggc tgttttgttt gaagctt 5917

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247 <210> SEQ ID NO: 2

248 <211> LENGTH: 501

249 <212> TYPE: DNA

250 <213> ORGANISM: Sus scrofa

253 <220> FEATURE:

254 <221> NAME/KEY: CDS

255 <222> LOCATION: (1)..(501)

256 <223> OTHER INFORMATION: Nucleotide sequence of the entire coding region of porcine

peptin

257 (i.e. signal peptide and secreted protein)

259 <400> SEQUENCE: 2

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260 atg cgc tgt gga ccc ctg tgc cga ttc ctg ctg gct ttg gcc tat ctg      48
261 Met Arg Cys Gly Pro Leu Cys Arg Phe Leu Leu Ala Leu Ala Tyr Leu
262 1          5          10          15
264 tcc tac gtt gaa gcc gtg ccc atc tgg aga gtc cag gat gac acc aaa      96
265 Ser Tyr Val Glu Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys
266          20          25          30
268 acc ctc atc aag acg att gtc acc agg atc agt gac att tca cac atg      144
269 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met
270          35          40          45
272 cag tct gtc tcc tcc aaa cag agg gtc acc ggt ttg gac ttc atc cct      192
273 Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
274          50          55          60
276 ggg ctc cat cct gtc ctg agt ttg tcc aag atg gac cag acc ctg gcg      240
277 Gly Leu His Pro Val Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
278 65          70          75          80
280 atc tac caa cag atc ctc acc agt ctg cct tcc aga aat gtg atc caa      288
281 Ile Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln
282          85          90          95
284 ata tcg aat gac ctg gag aac ctc cgg gac ctt ctc cac ctg ctg gcc      336
285 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
286          100          105          110
288 tcc tcc aag agc tgc ccc ttg ccc agc agg gcc ctg gag acc ttg gag      384
289 Ser Ser Lys Ser Cys Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu
290          115          120          125
292 agc ctg ggc ggc gtc ctg gaa gcc tcc ctc tac tcc acg gag gtg gtg      432
293 Ser Leu Gly Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
294          130          135          140
296 gcc ctg agc agg ctg cag ggg gct ctg cag gac atg ctg cgg cag ctg      480
297 Ala Leu Ser Arg Leu Gln Gly Ala Leu Gln Asp Met Leu Arg Gln Leu
298 145          150          155          160
300 gac ctc agc cct ggc tgc tga      501
301 Asp Leu Ser Pro Gly Cys,
302          165
305 <210> SEQ ID NO: 3
306 <211> LENGTH: 166
307 <212> TYPE: PRT
308 <213> ORGANISM: Sus scrofa
310 <400> SEQUENCE: 3
312 Met Arg Cys Gly Pro Leu Cys Arg Phe Leu Leu Ala Leu Ala Tyr Leu
313 1          5          10          15
316 Ser Tyr Val Glu Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys
317          20          25          30
320 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met
321          35          40          45
324 Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
325          50          55          60
328 Gly Leu His Pro Val Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
329 65          70          75          80
332 Ile Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln

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333      85      90      95
336 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
337      100      105      110
340 Ser Ser Lys Ser Cys Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu
341      115      120      125
344 Ser Leu Gly Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
345      130      135      140
348 Ala Leu Ser Arg Leu Gln Gly Ala Leu Gln Asp Met Leu Arg Gln Leu
349 145      150      155      160
352 Asp Leu Ser Pro Gly Cys
353      165
356 <210> SEQ ID NO: 4
357 <211> LENGTH: 166
358 <212> TYPE: PRT
359 <213> ORGANISM: Sus scrofa
362 <220> FEATURE:
-> 363 <221> NAME/KEY: Protein
364 <222> LOCATION: (1)..(166)
365 <223> OTHER INFORMATION: Amino acid sequence of the entire coding region of porcine
ptin
366      (i.e. signal peptide and secreted protein)
368 <220> FEATURE:
-> 369 <221> NAME/KEY: Protein
370 <222> LOCATION: (1)..(166)
371 <223> OTHER INFORMATION: Amino acid translation of the entire coding region of
rcine
372      leptin (i.e. signal peptide and secreted protein)
374 <400> SEQUENCE: 4
376 Met Arg Cys Gly Pro Leu Cys Arg Phe Leu Leu Ala Leu Ala Tyr Leu
377 1      5      10      15
380 Ser Tyr Val Glu Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys
381      20      25      30
384 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met
385      35      40      45
388 Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
389      50      55      60
392 Gly Leu His Pro Val Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
393 65      70      75      80
396 Ile Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln
397      85      90      95
400 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
401      100      105      110
404 Ser Ser Lys Ser Cys Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu
405      115      120      125
408 Ser Leu Gly Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
409      130      135      140
412 Ala Leu Ser Arg Leu Gln Gly Ala Leu Gln Asp Met Leu Arg Gln Leu
413 145      150      155      160
416 Asp Leu Ser Pro Gly Cys
417      165
420 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/03/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2943,2944,2983,3037

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11

VERIFICATION SUMMARY

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L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2940
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:3000
L:363 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:369 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:528 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:582 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:616 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9